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OM nucleic - nucleic search, using sw model

Run on: June 24, 1999, 01:30:23 ; search time 366.45 Seconds

Perfect score: 356 (without alignments)
Sequence: 1.tgaccctctggaaacctatc.....atctggagctgaaagaattc 356

Title: US-09-205-015-3
Scoring table: IDENTITY_NUC

Searched: 808301 seqs, 1788773984 residues

Database : GenEmbl:
1: gb_ba1:*

2: gb_da2:*

3: gb_ln:*

4: gb_on:*

5: gb_ov:*

6: gb_pat:*

7: gb_Dh:*

8: gb_p11:*

9: gb_p12:*

10: gb_pr1:*

11: gb_pr2:*

12: gb_pr3:*

13: gb_ro:*

14: gb_st:*

15: gb_sy:*

16: gb_un:*

17: gb_y1:*

18: gb_hng:*

19: em_ba:*

20: em_fun:*

21: em_hum1:*

22: em_hum2:*

23: em_in:*

24: em_on:*

25: em_or:*

26: em_ov:*

27: em_pat:*

28: em_ph:*

29: em_p1:*

30: em_ro:*

31: em_sy:*

32: em_un:*

33: em_v1:*

34: em_hcg:*

35: em_srs:*

36: gb_ba1:*

37: gb_ba2:*

38: gb_p11:*

39: gb_p12:*

40: gb_pr1:*

41: gb_pr2:*

42: gb_pr3:*

43: gb_sts:*

ALIGNMENTS

RESULT	1	10-JUL-1992
S49899	356 bp	DNA
LOCUS	alpha globin gene cluster: [5' region, major regulatory element]	
DEFINITION		
[human, Genomic, 356 nt.]		
ACCESSION		
NID	923377	
KEYWORDS		
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata; Chordata;	
REFERENCE	1 (bases 1 to 356)	
AUTHORS	Jarmain,A.P., Wood,W.G., Sharpe,J.A., Gourdon,G., Ayyub,H. and Higgs,D.R.	
TITLE	Characterization of the major regulatory element upstream of the human alpha-globin gene cluster	
JOURNAL	Mol. Cell. Biol. 11 (9), 4679-4689 (1991)	
MEDLINE	91342671	
REMARK	GenBank staff at the National Library of Medicine created this entry [NCBI glibsq 49899] from the original journal article. This sequence comes from fig 5.	
COMMENT	Region: alpha-globin gene cluster.	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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FEATURES Location/Qualifiers
 source 1. .356
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 89 a 89 c 108 g 70 t
 ORIGIN

Query Match 99.68; Score 354.4; DB 10; Length 356;
 Best Local Similarity 99.7%; Pred. No. 6.9e-103; Length 356;
 Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

repeat_region /note="AluJb repeat: matches 301. .5 of consensus"
 repeat_region /note="AlusX repeat: matches 1. .136 of consensus";
 incomplete repeat"
 repeat_region 1291. .1601
 repeat_region /note="AlusP repeat: matches 1. .300 of consensus"
 repeat_region /note="AlusG repeat: matches 132. .288 of consensus";
 incomplete repeat"
 repeat_region 3487. .3784
 repeat_region /note="AlusG repeat: matches 1. .299 of consensus"
 repeat_region 3809. .4104
 repeat_region /note="AluJb repeat: matches 1. .302 of consensus"
 repeat_region 4823. .5030
 repeat_region /note="AlusG repeat: matches 2. .208 of consensus";
 incomplete repeat"
 repeat_region 5053. .5092
 repeat_region /note="20 copies of 2 mer 85 % conserved"
 repeat_region 5122. .5280
 repeat_region /note="FAM repeat: matches 164. .5 of consensus"
 repeat_region 5759. .5903
 repeat_region /note="LIMC2 repeat: matches 169. .321 of consensus"
 repeat_region 6130. .6427
 repeat_region /note="AlusG repeat: matches 297. .1 of consensus"
 repeat_region 6428. .6724
 repeat_region /note="AluJb repeat: matches 299. .1 of consensus"
 repeat_region 7144. .7265
 repeat_region /note="LIMC2 repeat: matches 293. .169 of consensus"
 repeat_region 7453. .7747
 repeat_region /note="AlusP repeat: matches 1. .303 of consensus"
 complement(join(7979. .8064,10081. .10234,14760. .14834,
 16585. .16668))
 /codon_start-1
 /product="14 gene"
 /db_xref="PID:5300374"
 /db_xref="PID:91817580"
 /translation:"MCQQFELKLDNYRPTLQLHALGQISKTDSPKRKEAPTML
 LFNVVAFNARADPSVINCJHNUSSRITKADYR"
 ADGNGPQSFPHILPKCLARDKEADVR"

repeat_region 8094. .8307
 /note="AlusQ repeat: matches 212. .1 of consensus";
 incomplete repeat"
 repeat_region 8578. .8861
 /note="AluY repeat: matches 3. .297 of consensus"
 repeat_region 8907. .9210
 /note="AluJb repeat: matches 300. .1 of consensus"
 repeat_region 9807. .9887
 /note="MIR repeat: matches 105. .185 of consensus"
 repeat_region 12438. .12731
 /note="AluJb repeat: matches 297. .3 of consensus"
 repeat_region 12946. .13243
 /note="AlusP repeat: matches 299. .2 of consensus"
 repeat_region 14000. .14139
 /note="AluJb repeat: matches 2. .141 of consensus";
 incomplete repeat"
 repeat_region 14140. .14453
 /note="AlusX repeat: matches 1. .302 of consensus"
 repeat_region 14454. .14596
 /note="1LMB6 repeat: matches 760. .907 of consensus"
 repeat_region 16385. .16584
 /note="10 copies of 20 mer 91 % conserved"
 repeat_region 18800. .19089
 /note="AlusX repeat: matches 1. .293 of consensus"
 BASE COUNT 5242 a 4881 c 4603 g 4500 t
 ORIGIN

FEATURES Location/Qualifiers
 source 1. .19226
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="16"
 /map="10p13.3"
 /clone="G4"
 repeat_region 601. .894

Query Match 99.6%; Score 354.4; DB 11; Length 19226;
 Best Local Similarity 99.7%; Pred. No. 9.9e-103;
 Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 tcgaccctctggaaacctataaggaccacagtccggccaaacatctggccaaaggc 60

Search completed: June 24, 1999, 01:30:43

